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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/583,212	11/22/2006	Valerie Frankard	1187-30	2213
28249	7590	01/23/2009	EXAMINER	
DILWORTH & BARRESE, LLP			COLLINS, CYNTHIA E	
333 EARLE OVINGTON BLVD.				
SUITE 702			ART UNIT	PAPER NUMBER
UNIONDALE, NY 11553			1638	
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			01/23/2009	PAPER

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

<b>Office Action Summary</b>	<b>Application No.</b>	<b>Applicant(s)</b>
	10/583,212	FRANKARD ET AL.
	<b>Examiner</b>	<b>Art Unit</b>
	Cynthia Collins	1638

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

#### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

#### Status

1) Responsive to communication(s) filed on 31 October 2008.  
 2a) This action is **FINAL**.                    2b) This action is non-final.  
 3) Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

#### Disposition of Claims

4) Claim(s) 1-28 is/are pending in the application.  
 4a) Of the above claim(s) 1-3 and 15-28 is/are withdrawn from consideration.  
 5) Claim(s) \_\_\_\_\_ is/are allowed.  
 6) Claim(s) 4-14 is/are rejected.  
 7) Claim(s) 11 is/are objected to.  
 8) Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

#### Application Papers

9) The specification is objected to by the Examiner.  
 10) The drawing(s) filed on 16 June 2006 is/are: a) accepted or b) objected to by the Examiner.  
 Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
 Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).  
 11) The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

#### Priority under 35 U.S.C. § 119

12) Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).  
 a) All    b) Some \* c) None of:  
 1. Certified copies of the priority documents have been received.  
 2. Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.  
 3. Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

#### Attachment(s)

1) Notice of References Cited (PTO-892)  
 2) Notice of Draftsperson's Patent Drawing Review (PTO-948)  
 3) Information Disclosure Statement(s) (PTO/SB/08)  
 Paper No(s)/Mail Date 21207.

4) Interview Summary (PTO-413)  
 Paper No(s)/Mail Date. \_\_\_\_\_.  
 5) Notice of Informal Patent Application  
 6) Other: \_\_\_\_\_.

***Election/Restrictions***

Applicant's election with traverse of Group IX, claim(s) 4-14, drawn to a method for improving plant growth characteristics comprising introducing and expressing in a plant an isolated nucleic acid sequence encoding a GRUBX protein, or wherein said improved growth characteristics is increased yield or modified plant architecture, and SEQ ID NOs: 1 and 2, in the reply filed on October 31, 2008 is acknowledged.

The traversal is on the ground(s) that the single inventive technical feature linking the different groups is the previously unknown use of GRUBX molecule to improve plant growth characteristics, regardless of whether the use comprises increasing expression and/or activity and/or levels of the GRUBX molecule and regardless of whether the use is effected by site-directed mutagenesis, homologous recombination, TILLING and T-DNA activation or by any other method.

This is not found persuasive because the technical feature linking all of the groups of invention is a nucleic acid sequence encoding a UBX domain protein, which technical feature is not a special technical feature, as set forth at page 4 of the restriction requirement mailed August 29, 2008.

Claims 1-3 and 15-28 are withdrawn from consideration.

The requirement is still deemed proper and is therefore made FINAL.

***Claim Objections***

Claim 11 is objected to because of the following informalities: claim 11 is objected to because the preamble is grammatically incorrect. Appropriate correction is required. It is suggested that “The method according claim 10” be amended to “The method according to claim 10” in order to overcome the objection.

***Specification***

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. See, e.g. pages 10 and 39. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01.

***Claim Rejections - 35 USC § 112***

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 4-14 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The claimed method require the use of a broad genus of nucleic acid molecules encoding a GRUBX protein, including nucleic acid molecules isolated from a eukaryotic organism and nucleic acid molecules that are hybridizing variants, functional portions, alternative splice variants, or allelic variants of GRUBX encoding nucleic acid molecules or of SEQ ID NO:1, or that encode homologues, derivatives, and active fragments of GRUBX proteins or of SEQ ID NO:2.

The specification describes the structure of GRUBX proteins as comprising at least an UBX domain, preferably an UBX domain and a PUG domain, and optionally also a Zinc finger domain (page 6). The specification discloses that increasing seed yield, particularly the harvest index, is one of the activities of GRUBX proteins (page 7). The specification does not disclose what other specific activities GRUBX proteins exhibit.

With respect to nucleic acid molecules that encode proteins having both the structural and functional attributes of a GRUBX protein, the specification describes a single species, the nucleotide sequence of SEQ ID NO:1 encoding the amino acid sequence of SEQ ID NO:2, a nucleic acid isolated from *Nicotiana tabacum* that, when expressed from a seed-preferred prolamin promoter in rice plants transformed therewith, increases the harvest index (a measure of seed yield) of the transformed plants as compared to nontransformed control plants (pages 41-43).

The specification does not describe other nucleic acid molecules obtained from other sources that encode proteins having both the structural (comprise at least an UBX domain) and functional (increase seed yield) attributes of a GRUBX protein. The specification also does not describe nucleic acid molecules that are hybridizing variants,

functional portions, alternative splice variants, or allelic variants of GRUBX encoding nucleic acid molecules or of SEQ ID NO:1, or that encode homologues, derivatives, and active fragments of GRUBX proteins or of SEQ ID NO:2.

The Federal Circuit has clarified the application of the written description requirement to nucleotide sequences. The court stated that “A description of a genus of cDNAs may be achieved by means of recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus or of a recitation of structural features common to members of the genus, which features constitute a substantial portion of the genus.” See *University of California v. Eli Lilly and Co.*, 119 F.3d 1559, 1569; 43 USPQ2d 1398, 1406 (Fed. Cir. 1997). The court has also affirmed the PTO's applicable standard for determining compliance with the written description requirement, quoting from the PTO's Guidelines for Examination of Patent Applications Under the 35 U.S.C. 112, P1, “Written Description” Requirement, 66 Fed. Reg. 1099, 1106, where it is set forth that the written description requirement can be met by “show[ing] that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics ... i.e., complete or partial structure, other physical and/or chemical properties, functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics.” See *Enzo Biochem Inc. v. Gen-Probe Inc.*, 63 USPQ2d 1609, 1613 (CAFC 2002)

In the instant case Applicant has not described a representative number of species falling within the scope of the genus of nucleic acid molecules required to practice the claimed invention, which genus encompasses numerous undisclosed and uncharacterized nucleic acid molecules that encode proteins that are hybridizing variants, functional portions, alternative

splice variants, or allelic variants of GRUBX encoding nucleic acid molecules or of SEQ ID NO:1, or that encode homologues, derivatives, and active fragments of GRUBX proteins or of SEQ ID NO:2, nor the structural features unique to the genus that are correlated with increasing seed yield.

Claims 4-14 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for A method comprising introducing into and expressing in a plant under the control of a seed-preferred promoter a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 or encoding the amino acid sequence of SEQ ID NO:2, does not reasonably provide enablement for methods comprising introducing into and expressing in a plant other nucleic acid molecules encoding other proteins. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claims are broadly drawn to methods comprising introducing and expressing in a plant nucleic acid molecules that encode a GRUBX protein, including nucleic acid molecules isolated from a eukaryotic organism that encode a GRUBX protein, and including nucleic acid molecules that are hybridizing variants, functional portions, alternative splice variants, or allelic variants of GRUBX encoding nucleic acid molecules or of SEQ ID NO:1, or that encode homologues, derivatives, and active fragments of GRUBX proteins or of SEQ ID NO:2.

The specification discloses the isolation from *Nicotiana tabacum* of the nucleotide sequence of SEQ ID NO:1 encoding the amino acid sequence of SEQ ID NO:2 (page 39). The specification also discloses a method comprising introducing into rice plants and expressing,

from a seed-preferred prolamin promoter, a nucleic acid molecule (SEQ ID NO:1) that encodes the amino acid sequence of SEQ ID NO:2 (pages 39-40). The specification additionally discloses that transgenic rice plants produced by the method have an increased harvest index (a measure of seed yield) as compared to nontransformed control plants (pages 41-43).

The specification does not disclose other nucleic acid molecules obtained from other sources that encode proteins that comprise at least an UBX domain and that function to increase seed yield when expressed in a plant transformed therewith. The specification also does not disclose how to alter or modify the nucleotide sequence of SEQ ID NO:1 or the amino acid sequence of SEQ ID NO:2 such that their seed yield increasing activity is retained.

The full scope of the claimed invention is not enabled because the function of a sequence cannot reliably be predicted on the basis of its structure or its homology to other known sequences, including sequences encoding proteins that comprise UBX domains.

See, for example, Whisstock J.C. et al. (Prediction of protein function from protein sequence and structure. *Q Rev Biophys.* 2003 Aug;36(3):307-40. Review), who teach

“... prediction of protein function from sequence and structure is a difficult problem, because homologous proteins often have different functions. Many methods of function prediction rely on identifying similarity in sequence and/or structure between a protein of unknown function and one or more well-understood proteins. Alternative methods include inferring conservation patterns in members of a functionally uncharacterized family for which many sequences and structures are known. However, these inferences are tenuous. Such methods provide reasonable guesses at function, but are far from foolproof.” (Abstract)

Whisstock J.C. et al. also teach at page 309 that while the observation that similar sequences determine similar structures gives us general confidence in homology modeling, much less reliable is the widely held assumption that proteins with very similar sequences should by virtue of their very similar structures have similar functions. Whisstock J.C. et al. further teach at

page 309 that to reason from sequence and structure to function is to step on much shakier ground, that while many families of proteins contain homologues with the same function, the assumption that homologues share function is less and less safe as the sequences progressively diverge, and that even closely related proteins can change function through divergence to a related function or by recruitment for a very different function in such cases the assignment of function on the basis of homology in the absence of direct experimental evidence will give the wrong answer.

Whisstock J.C. et al. additionally teach at page 310 that a protein need not even change sequence to change function, as numerous proteins exhibit multiple functions in different cellular environments such that even if detailed in vitro studies on isolated proteins do identify a function we cannot be sure we know the molecule's full repertoire of biological activities, and that nonhomologous proteins may conversely have similar functions.

Whisstock J.C. et al. further teach that while general hints based on protein sequence, structure, genomics and interaction patterns may be useful in guiding experimental investigations of protein function,

"inferring protein function from knowledge of the function of a close homologue is like solving the clue of an American crossword puzzle. Finding the word that satisfies the definition may be difficult but the task in principle is straightforward. Working out the function of a protein from its sequence and structure is like solving the clue of a British crossword puzzle. It is by no means obvious which features of the definition are providing the real clues, as opposed to misleading ones. Also, for both types of puzzle and for the suggestion of a protein function, even if your answer appears to fit it may be wrong." (pages 311-312).

See also, for example, Buchberger A. et al. (The UBX domain: a widespread ubiquitin-like module. *J Mol Biol.* 2001 Mar 16;307(1):17-24), who teach that the UBX domain, originally identified in a member of the ubiquitin-associated domain family of proteins implicated in

ubiquitination, is a module of unknown function present in many eukaryotic proteins.

Buchberger A. et al. also teach that the UBX domain is found in a number of different proteins that appear to be unrelated to those involved in ubiquitination (page 17 column 2).

In the instant case the specification does not provide sufficient guidance with respect to which nucleic acid molecules obtained from other sources that encode proteins that comprise at least an UBX domain would function to increase seed yield when expressed in a plant transformed therewith and which would not. The specification also does not provide sufficient guidance with respect to how to alter or modify the nucleotide sequence of SEQ ID NO:1 or the amino acid sequence of SEQ ID NO:2 such that their seed yield increasing activity is retained. Absent such guidance one skilled in the art would have to isolate from different sources numerous different sequences encoding GRUBX proteins, and modify in a variety of different ways the nucleotide sequence of SEQ ID NO:1, and then each sequence for its ability to increase seed yield in a plant transformed therewith, in order to determine which of sequences meeting the structural limitations set forth in the claims, if any, would function in the same manner as SEQ ID NO:1. Such a trial and error approach to practicing the claimed invention would constitute undue experimentation.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 9 and 10, and claims dependent thereon, are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claims 9 and 10 are indefinite in the recitation

of “capable of hybridising”, as it is unclear whether the hybridization of the sequence to the nucleic acid is required by the claimed methods.

Claim 9, and claims dependent thereon, are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 9 is indefinite in the recitation of “is as represented by”, as it is unclear in what way SEQ ID NO:1 is representative of the required nucleic acid molecule, and it is unclear in what way SEQ ID NO:2 is representative of the required GRUBX protein.

Claim 10, and claims dependent thereon, are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Claim 10 is indefinite in the recitation of “related gene family members”, as it is unclear what the gene family members are related to, e.g. each other? a GRUBX protein?

#### ***Claim Rejections - 35 USC § 102***

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 4-7 and 9-10, are rejected under 35 U.S.C. 102(b) as being anticipated by INZE et al. (WO 03/085115, published 16 October 2003).

The claims are drawn to a method for improving plant growth characteristics, said method comprising introducing and expressing or overexpressing in a plant a nucleic acid molecule isolated from a eukaryotic organism that encodes a GRUBX protein, including a nucleic acid molecule of SEQ ID NO:1 isolated from the plant *Nicotiana tabacum* that encodes a GRUBX protein of SEQ ID NO:2 and a nucleic acid molecule capable of hybridizing to a GRUBX encoding nucleic acid.

INZE et al. teach a method comprising introducing and expressing or overexpressing in a plant a nucleic acid molecule isolated from the plant *Nicotiana tabacum* that comprises the nucleotide sequence of SEQ ID NO:1 and that encodes a protein comprising the amino acid sequence of SEQ ID NO:2 (See INZE et al.'s SEQ ID NO:61 and page 13 lines 23-26). The nucleic acid molecule taught by INZE et al. is capable of hybridizing to a GRUBX encoding nucleic acid because it comprises the nucleotide sequence of SEQ ID NO:1. See also the sequence alignment between Applicant's SEQ ID NO:1 and SEQ ID NO: 61 of INZE et al. below.

While INZE et al. are silent with respect to whether their method is "for improving plant growth characteristics", INZE et al. need not explicitly teach this limitation in order to anticipate the claimed invention, since the recitation in the preamble of claim 1 is an intended use for the claimed method, and thus not limiting.

RESULT 3  
AX927140  
LOCUS AX927140 1729 bp DNA linear PAT 19-DEC-2003  
DEFINITION Sequence 61 from Patent WO03085115.  
ACCESSION AX927140  
VERSION AX927140.1 GI:40247876

Art Unit: 1638

KEYWORDS .

SOURCE Nicotiana tabacum (common tobacco)

ORGANISM Nicotiana tabacum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; asterids; lamials; Solanales; Solanaceae; Nicotianoideae; Nicotianeae; Nicotiana.

REFERENCE 1

AUTHORS Inze,D. and Broekaert,W.

TITLE Identification and validation of novel targets for agrochemicals

JOURNAL Patent: WO 03085115-A 61 16-OCT-2003; CropDesign N.V. (BE)

FEATURES Location/Qualifiers

source 1. .1729

/organism="Nicotiana tabacum"

/mol\_type="unassigned DNA"

/db\_xref="taxon:4097"

ORIGIN

Query Match 100.0%; Score 1380; DB 2; Length 1729;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGTGACATGAAGGATAAAAGTCAAAGGGTTCATGAAAAAAAGTCACATCTTCTTCTTCA 60  
 |||||||  
 Db 276 ATGGGTGACATGAAGGATAAAAGTCAAAGGGTTCATGAAAAAAAGTCACATCTTCTTCTTCA 335

Qy 61 GGTAAGTTAAAGGCCAAGGTAGGGTTTGGGTGGTTCATCTTCTTCAGGACCTCAAAT 120  
 |||||||  
 Db 336 GGTAAGTTAAAGGCCAAGGTAGGGTTTGGGTGGTTCATCTTCTTCAGGACCTCAAAT 395

Qy 121 CATGTCAATAATTTTCATCACATCCCCAAATACAAGGCAAGATCAACAACCTTCATAT 180  
 |||||||  
 Db 396 CATGTCAATAATTTTCATCACATCCCCAAATACAAGGCAAGATCAACAACCTTCATAT 455

Qy 181 ACAAAAACTTCGCCCTCAAAACCAAGTAATTCTGATCAAAGAATTGAGAATATATGTGAA 240  
 |||||||  
 Db 456 ACAAAAACTTCGCCCTCAAAACCAAGTAATTCTGATCAAAGAATTGAGAATATATGTGAA 515

Qy 241 ATTCAAGTTCAACAAAAGTGAATCAAAGGATGGTTTGATCCATTGGTGAATTAGTCACT 300  
 |||||||  
 Db 516 ATTCAAGTTCAACAAAAGTGAATCAAAGGATGGTTTGATCCATTGGTGAATTAGTCACT 575

Qy 301 TCTGGGAAGAGAAACCCAAAAGGTATTCACTTACTAATGTGTTGAATGCCCTGCTGT 360  
 |||||||  
 Db 576 TCTGGGAAGAGAAACCCAAAAGGTATTCACTTACTAATGTGTTGAATGCCCTGCTGT 635

Qy 361 GGTAGTGGTTTGTGTTCTGAAGAAGAGGTGTCAACTCATATTGATAGCTGTTAAGTTCT 420  
 |||||||  
 Db 636 GGTAGTGGTTTGTGTTCTGAAGAAGAGGTGTCAACTCATATTGATAGCTGTTAAGTTCT 695

Qy 421 GAAGTGTCTTCAATTGGGAGTTGAAAGTAAAGTTGAAGTAAAGTAAAGTGAATTGGAAACA 480  
 |||||||  
 Db 696 GAAGTGTCTTCAATTGGGAGTTGAAAGTAAAGTTGAAGTAAAGTGAATTGGAAACA 755

Qy 481 TGTGTTAGTGCAATATGTTTCAGGGAAAGCCCTCAGAAGGGTCAGTTGAAGTGGTCATTAAG 540  
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 Db 756 TGTGTTAGTGCAATATGTTTCAGGGAAAGCCCTCAGAAGGGTCAGTTGAAGTGGTCATTAAG 815

Qy 541 TTGTTAAAGAATATTGTGAAGGAACCAAGAGAAATGCCAAGTTAGGAAAATAAGGATGGGG 600  
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 Db 816 TTGTTAAAGAATATTGTGAAGGAACCAAGAGAAATGCCAAGTTAGGAAAATAAGGATGGGG 875

Qy 601 AATCCAAAATAAAAGGTGCTATAGGTGATGTTGAGGAGGTGGAGCTATTGGAATT 660  
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 Db 876 AATCCAAAATAAAAGGTGCTATAGGTGATGTTGAGGAGGTGGAGCTATTGGAATT 935

Qy 661 GTTGGATTGAGTTGAAAGAAGAGGTGGGGAAATTGGGCTGTGATGGATGTTCTTCT 720  
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 Db 936 GTTGGATTGAGTTGAAAGAAGAGGTGGGGAAATTGGGCTGTGATGGATGTTCTTCT 995

Qy 721 GAAGAACAACTGTTATGCTTAAGAATGAGTTCACTCTGGAACCGAAGAAGGTTGAA 780  
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 Db 996 GAAGAACAACTGTTATGCTTAAGAATGAGTTCACTCTGGAACCGAAGAAGGTTGAA 1055

Qy 781 GAGTTGGCGTCCTTATCCCAAGTTAAGGCAGTGAAACCAGTTGAGCCGAAGAAGATTGAT 840  
 |||||||  
 Db 1056 GAGTTGGCGTCCTTATCCCAAGTTAAGGCAGTGAAACCAGTTGAGCCGAAGAAGATTGAT 1115

Qy 841 AGACAGATTGAGTGTCTTCTGTTCCGAGAGCGTAGCAGCAAAATTGAGCTACCT 900  
 |||||||  
 Db 1116 AGACAGATTGAGTGTCTTCTGTTCCGAGAGCGTAGCAGCAAAATTGAGCTACCT 1175

Qy 901 GATTCCTTAAACCTCTCACGTGAGGAATTGAGAAGAGAACGGAGAGATGAGGAAGAAG 960  
Db 1176 GATTCCTTAAACCTCTCACGTGAGGAATTGAGAAGAGAACGGAGAGATGAGGAAGAAG 1235  
Qy 961 AAATTAGAAGATTCCAAATTATTGATTCTAAATCTTATCGGGAAAAGCAGGCAAAGCT 1020  
Db 1236 AAATTAGAAGATTCCAAATTATTGATTCTAAATCTTATCGGGAAAAGCAGGCAAAGCT 1295  
Qy 1021 GCAAGAAAAGAGTACACAAAATCCATTATCCGTGTACAGTTCCAGATGGAGCATTGCTT 1080  
Db 1296 GCAAGAAAAGAGTACACAAAATCCATTATCCGTGTACAGTTCCAGATGGAGCATTGCTT 1355  
Qy 1081 CAAGGTGCTTCTACCTCGGAGCCAACACTAGTCTCTTATGAGTTGTGAGCGCAGCG 1140  
Db 1356 CAAGGTGCTTCTACCTCGGAGCCAACACTAGTCTCTTATGAGTTGTGAGCGCAGCG 1415  
Qy 1141 TTAAAGGAACCAAGCTTAGAGTCGAATTGTTACATCCGGTGTGTTAAAAAGCGGGTG 1200  
Db 1416 TTAAAGGAACCAAGCTTAGAGTCGAATTGTTACATCCGGTGTGTTAAAAAGCGGGTG 1475  
Qy 1201 ATTCcccATTTCCAGCTGCTGGGGAGAGGGCTGTAAACAGTTGAAGAGAGGATTGGTT 1260  
Db 1476 ATTCcccATTTCCAGCTGCTGGGGAGAGGGCTGTAAACAGTTGAAGAGAGGATTGGTT 1535  
Qy 1261 CCTGCAGCTCTACTCAAATTAAACCTATCGAACAGATTCTGTTGTTTACTGGTCTT 1320  
Db 1536 CCTGCAGCTCTACTCAAATTAAACCTATCGAACAGATTCTGTTGTTTACTGGTCTT 1595  
Qy 1321 TGTAATGAGCTCTTGAAATTAGCGAGCCCCCTCGAGACCGGATCAGTTGCTTCCCTCGTAA 1380  
Db 1596 TGTAATGAGCTCTTGAAATTAGCGAGCCCCCTCGAGACCGGATCAGTTGCTTCCCTCGTAA 1655

### ***Remarks***

No claim is allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Cynthia Collins whose telephone number is (571) 272-0794. The examiner can normally be reached on Monday-Friday 8:45 AM -5:15 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg can be reached on (571) 272-0975. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished

applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

/Cynthia Collins/  
Primary Examiner, Art Unit 1638

CC